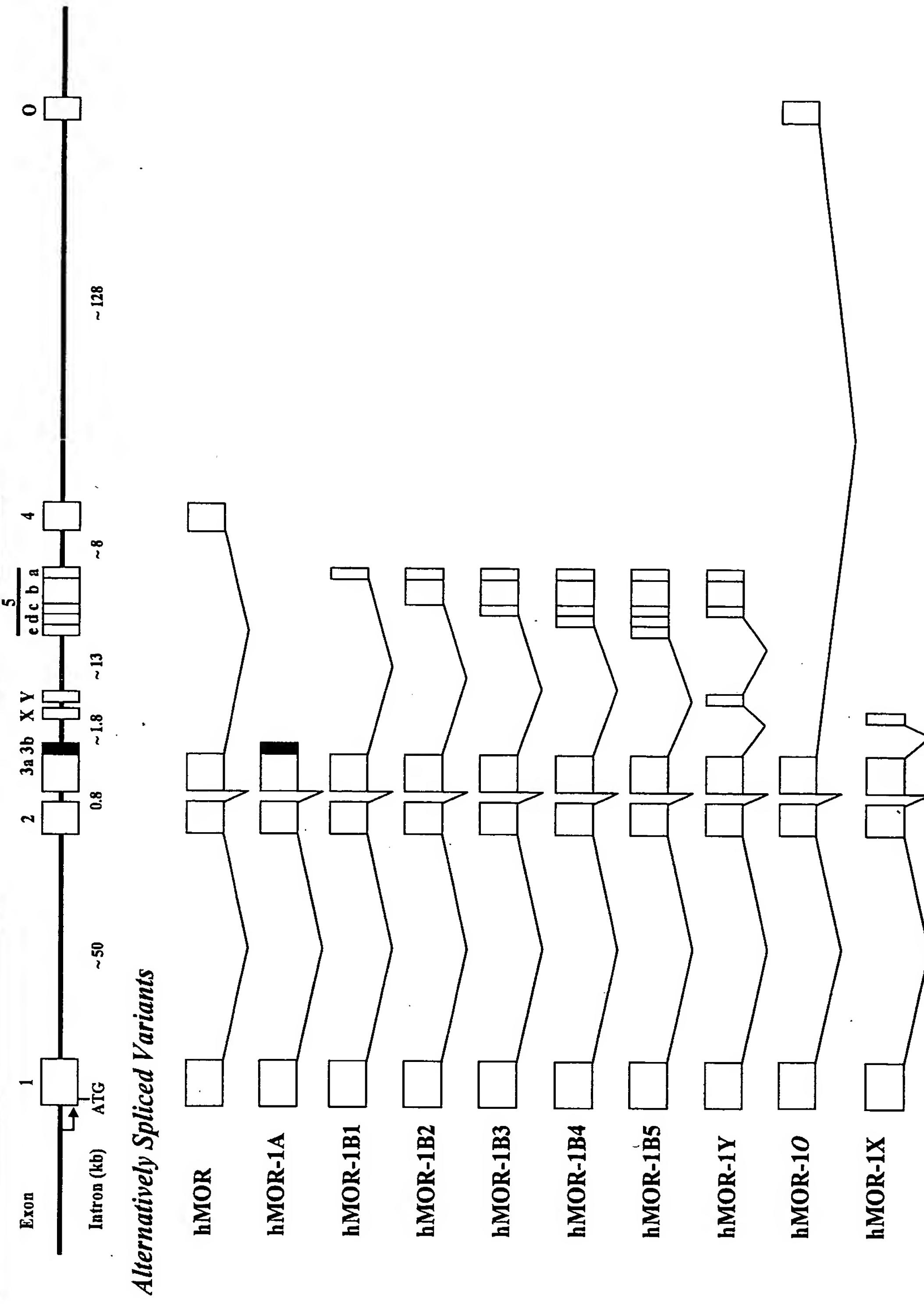


Genomic Structure of the human mu opioid receptor gene

FIG. 1

hBAC clone A (~130 kb)



hMOR-1A

Exon 3a ↓ **Exon 3b**

---ACTAATCATCAGGTACCGCAGTCTAGAATTAGGTATACTGGGATGACATAAAATTATAAGGCTT
 T N H Q V R S L * (SEQ ID NO: 27)
 TGTGCTAACTAGGAGTTAACATTAGAGGATGAGAATTAGAGGCTTAATCCATTAGAGGAAAGCAAGGG (SEQ ID NO: 28)

hMOR-1B1

Exon 3a ↓ **Exon 5a**

---ACTAATCATCAGAAAATAGATTATTCAAAGTCATCTTACTCAAACGTGAGCATACCAAGGGCTAATA
 T N H Q K I D L F Q K S[#] L N C E H T K G * (SEQ ID NO: 29)
 ATTACAAATATTTCCTCCGTGAAGAATAAGATTGAAAGC (SEQ ID NO: 30)

hMOR-1B2

Exon 3a ↓ **Exon 5b**

---ACTAATCATCAGAGAAAAGAACAGAGAAATCTGACTGGTAAGAAATTGTTACCCCTTTGCCAGGCATGCCA
 T N H Q R E R R Q K S[#] D W * (SEQ ID NO: 31)
 GGCTTCTGGGTTCCCTTCCCTGAGCGGCCCTAGTGATCCGGCTTGCGGCACCATCGGCC--- (SEQ ID NO: 32)

hMOR-1B3

Exon 3a ↓ **Exon 5c**

---ACTAATCATCAGGGACCCAGCCAAAGTTGCTTGACCAACTGCCGGTCGTCTTGAAGGGGGCTT
 T N H Q G P P A K F V A D Q L A G S S * (SEQ ID NO: 33)
 ACAGGTGTTCCAAGCCCCGTGTTTATCCTCAAGTATCCCTAACACAGAAAACGACCTCATACACAAAA--- (SEQ ID NO: 34)

hMOR-1B4

Exon 3a ↓ **Exon 5d**

---ACTAATCATCAGAGCTGACTATGACATGAACCCCTAAAAATT CCTGTTCCC--- (SEQ ID NO: 35)
 T N H Q S * (SEQ ID NO: 36)

FIG. 1B(1)

hMOR-1B5

Exon 3a ↓ **Exon 5e**

---ACTAATCATCAGGTGGAATTGAAACCTGGACTGTCACTGGAAATGCCAAAGCCTTGGCCACTGAGCTACAA
T N H Q V E L N L D C H C E N A K P W P L S Y* N
TGCAGGGTAGTCTCCATTCCCTCCAGGAAGAGTCTAGAGCTTA--- (SEQ ID NO: 37)
A G * (SEQ ID NO: 38)

hMOR-1Y

Exon 3a ↓ **Exon Y**

---ACTAATCATCAGAGATCCAATATCAAACCTCCCCAGGGTGTCTGTATTCTGACAACTGTCCACTGA
T N H Q I R D P I S N L P R V S# V F * (SEQ ID NO: 39)
↓ **Exon 5c**

GGCAATTCCATAACAGGGCAAAGTGGAGTTGGCAGTTATCAAGGGACCTCCAGCCAAAGTTTGTT--- (SEQ ID NO: 40)

3/26

FIG. 1B(2)

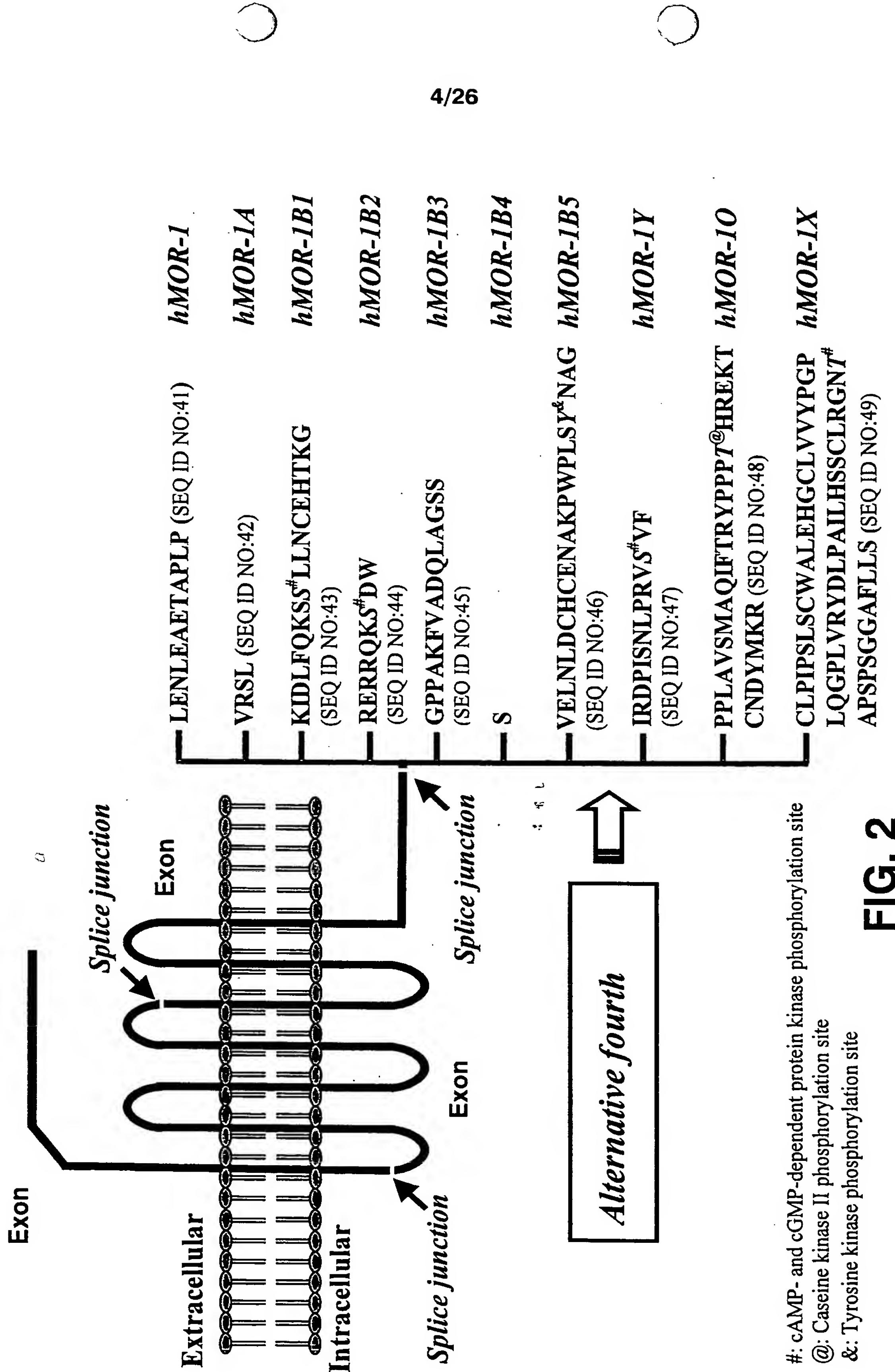


FIG. 2

hMOR-1B1 (1354 bp)

hMOR-1B1 (406 aa)

MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCCPNRTDLGGRDSLCPPTGSPPSMITA
GLFGNFLVMYVIVRYTKMKTATNNYIFNLALADALATSTLPFQSVNYYLMGTWPFGTILCKJVISIDY
YIAVCHPVKALDFRTPRNAKINVCNWLSSAIGLPVMMATKVRQGSIDCTLTFSHPTWYWENLL
CYGLMLRLKSVRMLSGSKEKDRNLRITRMVLVVAVFIVCWTPIHIYVIKALVTIPETTFQTVSWHF
CIALGYTNSCLNPVLYAFLDENFKRCFREEFCIPTSSNIEQQNSTRIRQNTRDHPSTANTVDRTNH
QKIDLFQKSSILLNCEHTKG (SEQ ID NO:51)

FIG. 3A

nMOR-1B2 (2218 bp)

CGGTGCTGGCTACCTCGCACAGCGGTGCCCCGGCTCAGTACCAAGGCAGGCCACGGCTGCCAACCG
CCAGGAATTGCACGTGATGGCTTGGGTTACTCAAGGCCCCAGCCTGGCTGGGTCAAACCTGGTCCC
CTTAGATGGCAACCTGTCCGACCCATGGGGTCCGAAACCGACCTGGGAGAGACAGCCTCCGGAC
CGGCAGTCCTCCATGATCACGGCATCACGGTCAAGATAACCCAGTGAAGAGACTGGCACCACATCTACATTTCAAC
TTCCCTGGTCATGTGATTGTGTCAGATAACCCAAGATGGAAACATGGGAACATGGCATTTCACATTTGGAACCACTCC
AGATGGCTTAGCCACCGTACCCCTGCCAGAGTGTGAATTACCTAATGGCAACCCATGGGACCTGGTGTGATCGAT
TGCAAGAGATAGTGATCTCCATAGATTACTATAACATGGTCAACCCGATATTCAACCCCTCTGCAACCTGGTGTG
ACATTGGCAGTGTGCCACCCCTGTCAAGGGCTTAGATTCCCGTACTCCCCGAAATGCCAAAATTATCAATGTCTGCAACTG
GATCCCTCTTCAGCCATTGGCTCATGGCTCATGGTCAACACAAAATACAGGCAAGGTCCATAGATGGTACAC
TAACATTCTCATCCAAACCTGGTACTGGGAAACCTGGCTGAAGAGATCTGGTTTCATCTGCCCTCATATTGCCAGTG
CTCATCATTACCGGTGTGCTATGGACTGATGATGATCTGGCCTCAAGAGTGTCCGCTCAAGAGTGTGGCTCTGGCT
ACAGGAATCTTCGAAAGGATCACCGGATGGGTGGCTGGTGTGTTCAATGGGACTCCATGGTCTGCACTTCTGGC
TTACGGTCATCATTAAAGGCCCTGGTTACAATCCCAGAAACTACGGTTCCAGACTGGTCTGGCAACTTCTGGC
GTTACACAAACAGCTGCCTCAACCCAGTCCATTGGCATTTCTGGATGAAAACACTCAAACGATGCTCAGAGAGTTCTG
TATCCCAACCTCTCCAAACATTGGCAACAAACTCCACTCGAATTCTGTCAGAACACTAGAGACCACCCCTCACGGCC
AATACAGTGGATAAGAACATAATCAGAGAGAAAGAACAGAAATCTGACTGGTAAGGAATTTGTTACCCCTTGCCA
GCATGCCAGGGCTTCTGGGTCCCTGAGGGCCCTAGTGATCCGGCTTGCGGCACCATGCCCTACGGCCAAAGC**6/26**
TGCATCATAAAGGAAATTTCATTCTGGCCAGAGCAAACACATGTGATAAAACATAGGCATTTAGCTACTCTG
CTTAGCACCAAATATCAGACTAGCTTAAATTGGCCCTTACATCTGGTCCATCATTAACTCGAACCTCTGACCTTGCA
TTCAACACGGTGTCTTGGCAAAACAGTGGCTGGGAAAGGTGAAATGATCAAGGGAGGGCAGAGAAAGACTCACCT
AATGTGCCAGGGCTTCTGGGTGGGAAAGGATCTGGCTGGGAAAGGAAAGGAAAGACTCACCTATTGGCAGCAACACT
GTAGAAAGTTCAGGCAAGGGTGGCTGGGAAAGGATCTGGCTGGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAG
GGGAGGAAAAAGCTCCCCATGTCCCCGATCCTGTCATGGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAG
AGACAGGATTAAATCCAAGGAGAATAGCAATTAAATCCCATAGCATAAAAGCTGTTAGCCAAAGGGGACTTTAAC
GGAGGGGTCTAACACCCCTAAATCTTAGAAGAGACTCTAACAGTTGCAATCCATGGGAGGAATGCTTGTGATAAGATA
TTAATTGACTCCCCATCTAACAGTTGCAATCCATGGGAGGAATGCTTGTGATAACCTCGGGTGTGATAAGATA
ATACATAGAAGTGTGAGGAGGTAGCATAAGAAATAACAGTAGTTAGAGAAAATTAGTCCAAACTATAGAA
ACATAGAATGTGAGGAGGTAGCACAATAAGGAAATAAGTCAATTGAGGATTATTGATGATAAAA
GCCATCTAAC (SEQ ID NO:52)

FIG. 3B(1)

hMOR-1B2 (397 aa)

MDSSAAPTNASNCTDALAYSSCCSAPSPGSWVNLSHLDGNLSDPCGNRTDLGGRDSLCPPTGSPSMSMITAITIMALYSIVCVV
GLFGGNFLVMYVIVRYTKMKTATNIYIFNLALADALATSTLPFQSVNYLMIGTWPFGTILCKIVISIDYYNMFTSIFTLCCTMSVDR
YIAVCHPVVKALDFRTPRNAKINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLFSHPTWYWENLLKICVFIIFAFIMPVLITY
CYGLMILRLKSVRMLSGSKEKDRLNLRITRMVLVVVAVFIVCWTPHIYVIKALVTIPETTFQTVSWHFCLALGYTNSCLNPV
LYAFLDENFKRCFREFCIPTSSNIEQQNSTRIRQNTRDHPSTANTVDRTNHQRERRQKS DW
(SEQ ID NO:53)

7/26

FIG. 3B(2)

hMOR-1B3 · (2483 bp)

FIG. 3C(1)

FIG. 3C(2)

9/26

GTCCAAACTAACATAAGAATGTGAGAGGCACATAAGAAATAAGTCATGGGGATTTCAT
GGACCAGCAATAATGATGATAAAAGCCATCTAAC (SEQ ID NO:54)

hMOR-1B3 (403 aa)

MDSSAAPTNASNCITDALAYSSCCSPAPSPGSWVNLSHLDGNNLSDP
CGPNRTDLCGRDSLCPPTGSPSMITAITIMALYSIVCVV
GLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALATSTL
PFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLC
YIAVCHPVKAIDFRTPRNAKINVCNWLSSAIGLPVMM
CYGLMILRLKSVRMLSGSKEKDRLNLRTRMVLVVVA
LYAFLDENFKRCFREFCIPTSSNIEQQNSTRIRQNTRD
HPSTANTVDRTNHQGPPAKFVADQLAGSS (SEQ ID NO:55)

hMOR-1B4 (1251 bp)

CGGTGCTCCTGGCTACCTCGGACTTGGCTACTGCCCTTGCTCAAGTTGGTCAACTTGGCTCCCA
CCAGCAATTGGCACTGCAACCTGCCATGGGCCCCATGCCGACAGCCGGCTGGGAGACAGGAGA
CGGCAGTCCCTCATGCCATCGGATCACGGATTCAGCTGGCTACTCCATCGTGTGGCTCTGGC
TTCTGGTCATGTGATGTGCTCAGATAACAGATAACCCAGTACCGTACCCCTGGCTCCAGAG
AGATGCCATTAGCCACCAGTACCTAACCTAATGGAACATGCCATTGGCTGAAATTACCT
TGCAGATTACTACATGAGTGTGATGCACCATGGCATACTGGCTCAGCATGGCTAG
ACATTGCAGTCTGCCACCCCTGTAAGGGCTTAGATTTCCGGTACTGCCAAATTCAAT
GATCCTCTCCAGCCATTGGCTCATGGCTACAAACAAATAACAGGAAGGCAAGG
TAACATTCTCATCCACCTGGTACTGGGAAACCTGCTGAAGAGATCTGGCTCAT
CTCATTCAGTGGACTGATGATGCTGGCTCTGGCTCCAGAGTCTGGCTCAT
ACAGGAATACTTCGAAGGGATCACCGAGATGGCTGGGACTCCCATTACACAT
TTACGTCAATTAAAGCCTTGGTTACAATCCCAGAAACTACGGTTCTGGC
GTTACACAAACAGCTGCCCTCAACCCAGTCATTGCATTCTGGGATGCTG
TATCCCAACCTCCAAACATTGAGCAACTCGAATTAGAGACCATGACT
AATACAGTGGATAGAAACTAATCGAACATGACTGAGCTGGCTCCACGGCC
(SEQ ID NO:56)

hMOR-1B4 (389 aa)

10/26

MDSSAAPTNASNCTDALAYSSCSPAPSPGSSWVNLSHLDGNLSDPCGPNRTDLCGRDSLCPPTGSPSMITAITIMALYSIVCVV
GLFGNFLVMYVIVRYTKMKTATNIYVFNLALADALATSTLPFQSVNYLMGTPFGTILCKIVVISIDYYNMFTSIFTLCTMSVD
RYIAVCHPVKALDFRTPRNAAKINVCNWLSSAIGLPVMMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPVLIT
VCYGLMRLKSVRMLSGSKEKDRNLRRJTRMVLVVAVFIVCWTPHIYVIKALVTIPETTFQTVSWHFICIALGYTNNSCLNPK
VLYAFLDENFKRCREFCIPTSSNIEQQNSTRIRQNTRDHPSTANTVDRTNHQS (SEQ ID NO:57)

FIG 3D

hMOR-1B5 (1402 bp)

CGGTGCTCCTGGCTACCTCGCACAGGGTCCCCGGTCAGTACCCAGCAGCCCCAGCAGTGGCTTAAGTTGACTCAAGTTGCTTGGCTACTCCAGCAATTGGCACTTGATGCCACTGGCAACCTGTCCGACCCATGCGGTCCGAACCGCACCCTGACCTGGGAGACAGCAGCCCTACTCCATGGCCCATCAGCGATCATGGCCCTACTCCATGGCTGGGGCTTGGAAACCTGGCTCATGTGATTGTGATTGTGAGATAACCCAAGATGAAGACTGCCACCAACATCTACATTTCACCTAACCTAATGGGAACATGGCCATTGGAACCATCCTTGCAAGATAAGTGAATTACTATAACATGGCATATTCAACCCATTGACCATGTCACCTCTGCACCATGAGTGGTGTGATGGATACATTGCGAGTCTCCGTTAGATTCCGAAATGCCAAATATTACAATGCTGCAACTGATCCTCTCAGGCCATTGGCTCTGTCAAGGGCCTTAGATTCCGTAACCAAACAAATACAGGGCAAGGTCCCATAGATTGTACACTGTAACATTCTCATCCTAACCTGGGAAACCTGGTACTGGGACTCTGGCTCATCTCGCCCTCATCTGGAGATCTGTGTTTCATCTCGCCCTCATTATGCCAGTGCTCATTCATTACCGTGTGCTATGGGACTGATGATCTGGCCCTCAAGAGTGTCCGGCATGGCTCTGTGCTGGACTCTGCATTGCTCATCGTCTGCTGGCTGTGTTCATCGTCTGCACTTCTGCATTGCTCTGTTACCGTCACTTCCAGGATGCCAGGATCGAAGGATCAACCGTCTGGTTACAATCCCAGAAACTACGGTCCAGACTGTTCAACCGATGCTTCAAGAGTCTGTTCTGGACTCTGCATTGCTCATCGTCTGGCTTATGCAATTCTGGATGAAACACTAGAGACCACCCCTCCACGGCCATTCCCAACCTCTCCAAACAAACTCCACTCGAATTCTGCTCAGAACAACAGCTGCCTCAACCCAGTCCCTTATGCAATTCTGGATGAAACACTAGAGACCACCCCTCCACGGCTATCCAGCAGCTGGGATAGAAACTAATCATCAGGGTGGAAATTGAAACCTGGACTGTCACTGTGAAAGGACTCTGCAAGGCTTGGCCACTGAGCTACAATGGCAGGGTAGTCTCCATTCCCTGGTTAATTGAGCTTAATTGAGTTGGCAAGGGCTGTGAACTATGACATGAACCCATAATGGCTTCC (SEQ ID NO:58)

hMOR-1B5 (410 aa)

11/26

MDSAAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCGPNRRTDLGGRDSLCPPTGSPSMSITAITIMALYSIVCWWGLFGNFLVMMYVIVRYTKMKTATNIYIFNLALADALATSTLPFQSINYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCHPVVKALDFRTPRNKINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWEVLLKJCVFIFAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRIRTRMVLVVVAVFIVCWTPHIYVIKALVTIPETTFQTVSWHFCIALGYTNNSCLNPVLYAFLDENFKRCREFCIPPTSSNIEQQNSTRIRQNTRDHPSTANTVDRTNHQVELNLDCHCENAKPWPPLSYNAG (SEQ ID NO:59)

FIG. 3E

hMOR-1Y (2601 bp)

FIG. 3F(1)

FIG. 3F(2)

AGTTGCAATCCATGGAGGAATGCTTGATAACCTCGGTGATAAGATAAAAAACCAAGCATACTAGAAGTGTCTCTAAA
ATAAAAATACAGTAGTTGCTAGAGAAAATTAGTCACAAACTATAGAAACATAGAATGTGAGAGGTAGC
ACATAAGAAATAAGTCATGGGGATTATTTCATGGACCAGCAATATGATGATAAAAGCCATCTAACCAAGGGC
(SEQ ID NO:60)

hMOR-1 Y (402 aa)

MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCCGPNRTDLCGRDSLCPPTGSPSMSITAITIMALYSIVCVV
GLFGNFLVMMYVIVRYTKMKTATNIYIFNLALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDR
YIAVCHPVPKALDFRTPRNAKINVCNWLSSAIGLPVMFMATKVRQGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPVLITV
CYGLMILRLKSVRMLSGSKEKDRNLRIRTRMVLVVVAVFIVCWTPHIYVIKALVTIPETTFQTVSWHFCLALGYTNNSCLNPV
LYAFLDENFKRCFREFCIPPTSSNIEQQNSTRIRQNTRDHPSTANTVDRTNHQIRDPISNLPRVSVF (SEQ ID NO:61)

hMOR-1 (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDP
 hMOR-1A (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDP
 hMOR-1B1 (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDP
 hMOR-1B2 (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDP
 hMOR-1B3 (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDP
 hMOR-1B4 (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDP
 hMOR-1B5 (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDP
 hMOR-1O (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDP
 hMOR-1X (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDP
 hMOR-1Y (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDP
 Consensus (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDP

120
61

hMOR-1	(61)	PTGSPSMITAITIMALYSIVCWGLFGNFLVMMVVRYTCKMKTATNIYIFNLALADALAT
hMOR-1A	(61)	PTGSPSMITAITIMALYSIVCWGLFGNFLVMMVVRYTCKMKTATNIYIFNLALADALAT
hMOR-1B1	(61)	PTGSPSMITAITIMALYSIVCWGLFGNFLVMMVVRYTCKMKTATNIYIFNLALADALAT
hMOR-1B2	(61)	PTGSPSMITAITIMALYSIVCWGLFGNFLVMMVVRYTCKMKTATNIYIFNLALADALAT
hMOR-1B3	(61)	PTGSPSMITAITIMALYSIVCWGLFGNFLVMMVVRYTCKMKTATNIYIFNLALADALAT
hMOR-1B4	(61)	PTGSPSMITAITIMALYSIVCWGLFGNFLVMMVVRYTCKMKTATNIYVFNLALADALAT
hMOR-1B5	(61)	PTGSPSMITAITIMALYSIVCWGLFGNFLVMMVVRYTCKMKTATNIYIFNLALADALAT
hMOR-1O	(61)	PTGSPSMITAITIMALYSIVCWGLFGNFLVMMVVRYTCKMKTATNIYIFNLALADALAT
hMOR-1X	(61)	PTGSPSMITAITIMALYSIVCWGLFGNFLVMMVVRYTCKMKTATNIYIFNLALADALAT
hMOR-1Y	(61)	PTGSPSMITAITIMALYSIVCWGLFGNFLVMMVVRYTCKMKTATNIYIFNLALADALAT
Consensus	(61)	PTGSPSMITAITIMALYSIVCWGLFGNFLVMMVVRYTCKMKTATNIYIFNLALADALAT

14/26

FIG. 4(1)

15/26

180
121

hMOR-1	(121)	STLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCHPVKALDF
hMOR-1A	(121)	STLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCHPVKALDF
hMOR-1B1	(121)	STLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCHPVKALDF
hMOR-1B2	(121)	STLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCHPVKALDF
hMOR-1B3	(121)	STLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCHPVKALDF
hMOR-1B4	(121)	STLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCHPVKALDF
hMOR-1B5	(121)	STLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCHPVKALDF
hMOR-1O	(121)	STLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCHPVKALDF
hMOR-1X	(121)	STLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCHPVKALDF
hMOR-1Y	(121)	STLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCHPVKALDF
Consensus	(121)	STLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCHPVKALDF

240
1181

hMOR-1	(181)	RTPRNAKIIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1A	(181)	RTPRNAKIIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1B1	(181)	RTPRNAKIIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1B2	(181)	RTPRNAKIIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1B3	(181)	RTPRNAKIIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1B4	(181)	RTPRNAKIIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1B5	(181)	RTPRNAKIIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1O	(181)	RTPRNAKIIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1X	(181)	RTPRNAKIIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1Y	(181)	RTPRNAKIIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
Consensus	(181)	RTPRNAKIIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI

FIG. 4(2)

241

- 300

hMOR-1 (241) FAFIMPVLIIITVCYGLMILRLKSVRMLSGSKEKDRNLRRITRMVLVVVAVFIVCWTPIHI
hMOR-1A (241) FAFIMPVLIIITVCYGLMILRLKSVRMLSGSKEKDRNLRRITRMVLVVVAVFIVCWTPIHI
hMOR-1B1 (241) FAFIMPVLIIITVCYGLMILRLKSVRMLSGSKEKDRNLRRITRMVLVVVAVFIVCWTPIHI
hMOR-1B2 (241) FAFIMPVLIIITVCYGLMILRLKSVRMLSGSKEKDRNLRRITRMVLVVVAVFIVCWTPIHI
hMOR-1B3 (241) FAFIMPVLIIITVCYGLMILRLKSVRMLSGSKEKDRNLRRITRMVLVVVAVFIVCWTPIHI
hMOR-1B4 (241) FAFIMPVLIIITVCYGLMILRLKSVRMLSGSKEKDRNLRRITRMVLVVVAVFIVCWTPIHI
hMOR-1B5 (241) FAFIMPVLIIITVCYGLMILRLKSVRMLSGSKEKDRNLRRITRMVLVVVAVFIVCWTPIHI
hMOR-1O (241) FAFIMPVLIIITVCYGLMILRLKSVRMLSGSKEKDRNLRRITRMVLVVVAVFIVCWTPIHI
hMOR-1X (241) FAFIMPVLIIITVCYGLMILRLKSVRMLSGSKEKDRNLRRITRMVLVVVAVFIVCWTPIHI
hMOR-1Y (241) FAFIMPVLIIITVCYGLMILRLKSVRMLSGSKEKDRNLRRITRMVLVVVAVFIVCWTPIHI
Consensus (241) FAFIMPVLIIITVCYGLMILRLKSVRMLSGSKEKDRNLRRITRMVLVVVAVFIVCWTPIHI

301

hMOR-1 (301) YVIIKALVTIPETTFQTVSWHFCIALGYTNNSCLNPVLYAFLDENFKRCFREFCIPPTSSNI
hMOR-1A (301) YVIIKALVTIPETTFQTVSWHFCIALGYTNNSCLNPVLYAFLDENFKRCFREFCIPPTSSNI
hMOR-1B1 (301) YVIIKALVTIPETTFQTVSWHFCIALGYTNNSCLNPVLYAFLDENFKRCFREFCIPPTSSNI
hMOR-1B2 (301) YVIIKALVTIPETTFQTVSWHFCIALGYTNNSCLNPVLYAFLDENFKRCFREFCIPPTSSNI
hMOR-1B3 (301) YVIIKALVTIPETTFQTVSWHFCIALGYTNNSCLNPVLYAFLDENFKRCFREFCIPPTSSNI
hMOR-1B4 (301) YVIIKALVTIPETTFQTVSWHFCIALGYTNNSCLNPVLYAFLDENFKRCFREFCIPPTSSNI
hMOR-1B5 (301) YVIIKALVTIPETTFQTVSWHFCIALGYTNNSCLNPVLYAFLDENFKRCFREFCIPPTSSNI
hMOR-1O (301) YVIIKALVTIPETTFQTVSWHFCIALGYTNNSCLNPVLYAFLDENFKRCFREFCIPPTSSNI
hMOR-1X (301) YVIIKALVTIPETTFQTVSWHFCIALGYTNNSCLNPVLYAFLDENFKRCFREFCIPPTSSNI
hMOR-1Y (301) YVIIKALVTIPETTFQTVSWHFCIALGYTNNSCLNPVLYAFLDENFKRCFREFCIPPTSSNI
Consensus (301) YVIIKALVTIPETTFQTVSWHFCIALGYTNNSCLNPVLYAFLDENFKRCFREFCIPPTSSNI

16/26

FIG. 4(3)

361

420

hMOR-1 (361) EQQNSTIRQNTRDHPSTANTVDRTNHQLENLEAETAPLP-----
hMOR-1A (361) EQQNSTIRQNTRDHPSTANTVDRTNHQVRSL-----
hMOR-1B1 (361) EQQNSTIRQNTRDHPSTANTVDRTNHQKIDLFQKSSLNCEHTKG-----
hMOR-1B2 (361) EQQNSTIRQNTRDHPSTANTVDRTNHQRRRQKSDW-----
hMOR-1B3 (361) EQQNSTIRQNTRDHPSTANTVDRTNHQGPPAKFVADQLAGSS-----
hMOR-1B4 (361) EQQNSTIRQNTRDHPSTANTVDRTNHQSHQS-----
hMOR-1B5 (361) EQQNSTIRQNTRDHPSTANTVDRTNHQVELNLDCHCENAKPWPLSYNAG-----
hMOR-1O (361) EQQNSTIRQNTRDHPSTANTVDRTNHQPPLAVSMAQIFTRYPPPTHREKTCDYMKR--
hMOR-1X (361) EQQNSTIRQNTRDHPSTANTVDRTNHQCLPIPSLSCWALEHGCLVVYPGPLQGPLVRYD
hMOR-1Y (361) EQQNSTIRQNTRDHPSTANTVDRTNHQIRDPISNLPRVSVF-----
Consensus (361) EQQNSTIRQNTRDHPSTANTVDRTNHQ

17/26

421 446

hMOR-1 (401) ----- (SEQ ID NO:62)
hMOR-1A (393) ----- (SEQ ID NO:63)
hMOR-1B1 (407) ----- (SEQ ID NO:51)
hMOR-1B2 (398) ----- (SEQ ID NO:53)
hMOR-1B3 (404) ----- (SEQ ID NO:55)
hMOR-1B4 (390) ----- (SEQ ID NO:57)
hMOR-1B5 (411) ----- (SEQ ID NO:59)
hMOR-1O (419) ----- (SEQ ID NO:64)
hMOR-1X (421) LPAILHSSCLRGNATAPS PSSGAFLLS (SEQ ID NO:65)
hMOR-1Y (403) ----- (SEQ ID NO:61)
Consensus (388) ----- (SEQ ID NO:66)

FIG. 4(4)

rMOR-1A

Exon 3a ↓ **Exon 3b**

-----AACCACCGGTATGCTTCTAGAATTACGGATAACATAAAATAACCATACTGGTA
 N H Q V C A F * (SEQ ID NO: 67)
 CCAGTCTAAGATTAAATCTTTAANGAAGGTCAACTGAGGCCAAAGTCC (SEQ ID NO: 68)

rMOR-1C1

Exon 3a ↓ **Exon 7**

-----AACCACCGCCAGCCCTGGCAGTCAGCGTGGCCCCAGATCTTACAGGATATCCTTCTCCG
 N H Q P A L A V S V A Q I F T G Y P S P

↓ **Exon 8**

ACTCATGGTGAACACCTGCAAGAGTTACAGGGACAGACCTAGACCCTAGACGGTGGAAAGAACGTGGT
 T[□] H G E K P C K S[□] Y R D R P R P C G R T W
 CTTTGAATCGCGTGCAGAATCCAATGTGGAGCACTTCCATTGTGGAGCCGCATTAAATCTATAAA
 S[↑] L K S[□] R A E S[□] N V E H F H C G A A L I Y N

↓ **Exon 9a**

CAATGTGAATTTCATCTAAACACAGGGATGTGCTAGTGAGTTGGAGGTGCAGGC (SEQ ID NO: 69)
 N V N F I * (SEQ ID NO: 70)

FIG. 5(1)

rMOR-1C2

Exon 3a ↓ **Exon 7**
----AACCACGCCAGCCCTGGCAGTCAGCGTGGCCAGATCTTTACAGGATATCCTCTCCG
N H Q P A L A V S V A Q I F T G Y P S P
↓ **Exon 8**
ACTCATGGTGA^AACCCCTGCAAGAGTTACAGGGACAGACCTAGACCCCTGTGGAAAGAACGTGGT
T^D H G E K P C K **S^D** Y R D R P R P C G R T W
CTTTGAAATCGCGTGCAGAATCCAAATGTGGAGCACATTCCATTGTGGAGCCGATTAATCTATAA
S^D L K **S^D** R A E **S^D** N V E H F H C G A A L I Y N
↓ **Exon 9b**
CAATGA^ACTAAAATAGGCCAGTGTCCCTGGCTCCAGATGGCTGCACGTCGCTCGTGCCCC
N E L K I G P V S W L Q M P A H V L V R P
TGGTAATGAACACGGGCTCCGATTCTGAATAATCCTCTGTG (SEQ ID NO:71)
W * (SEQ ID NO:72)

rMOR-1D

Exon 3a ↓ **Exon 8**
----AACCACGCCAGACCTAGACCCCTGTGGAAAGAACGTGGTCTTGAATCGCGTGCAGAATCCAA
N H Q T * (SEQ ID NO:73) ↓ **Exon 9b**
TGTGGAGCACTCCATTGTGGAGGCCGATTAATCTATAACAATGAACTA^AAAATAGGGCCAGTG
TCCTGGCTCCAGATGCCTGGCAGCTGGCTGGTAATGAACACGGGGCTCCGATTC
TGAATAATCCTCTGTG (SEQ ID NO:74)

FIG. 5(2)

rMOR-1B2

Exon 3a → Exon 5b

N H Q E P Q S V E T * (SEQ ID NO : 75)
----AACCACGGAGGCCCTCAGTAGAGACATGATGTGAATGAACCAACTGATTAAACAAAG
GTTTCTGAACACTGAAATAACAAACAAATGTAGAGGTACTAGAGAAAATTGTAGCCCTGAAATTACGGAAACCAAATGAGT
GTGAGTGTATACATTTAAGGCCTCAGAGAGATTTCATGACTAACAAACATGACCCAAAGCACCTAAACTGTGGTGATTAGATTAA
CAAAGACAATTCTAGAGGCCCTGGGACTAAAGAAATTGTAGCCCTCACACACTCAGTAATGGAATGAGCAAATTAGA
TTAGTGAGAAAGATGGAGGAAGACTCGAAATATTTCATATCTTCATATCTTCAGAAACTCCACAAGAAAACCAATAAGAATAACCTGTC
TGGACCCCTTGGTGGCTTAC (SEQ ID NO : 76)

rMOR-1E

Exon 3a → Exon E

N H Q G A E L * (SEQ ID NO : 77)
----AACCACGGAGGCCCTTGGCCCCACAAATGGTAGGGCTCCCACACTCACACATCTCACTGTTCCCTTGT
AGCAGGCCAGGGAGGCCCTTGGCTTACGGCCATAGGCCATTCTGACTGACCTCAGATTATGCAATAACACCTAGATGGATCCGCCCTCA
TTTCAGCTATGGCTAACCGGCATACCGAAGTGGAAAGTGTGGCTTAATGCAATAACACGTGAGCCACACCCAGAGGCATGGTGAATGGCG
GGAGACAGGAATGCTCATACCGAAGTGGAAAGTGTGGCTTAATGCAATAACACGTGAGCCACACCCAGAGGCATGGTGAATGGCG
GCAGAGTCATCCCCACTCAAAGCAATTATAACAAATTATCTCCCTGCTTCCAGCTCAGAAATCAGAGCCAGACAGACAAATGGTT
CTCTGTTGCCCT
CTTTCTAAGCAGCCCTCTTAGGGTTCAAACACTCGCCCTGCACATTGGTAAAGGATTAAATTGATTTTGTCTCTCTCTCTCTCTCTCT
TTTCTCCAACCCAGGGATAAACATTAGAGCAAGGAAGAGGCATAGGAAGGCTTCCCTAGGTGTCCCTGCTTGCCTGACCCACCTGACCT
TGCTTTCAATTGGAGAAAGCAATTGAAACTATCTGAGCTTCAAATCTTGGCATTAAATATT
TGCTTTCAATTGGAGAAAGCAATTGAAACTATCTGAGCTTCCCTAGGTGTCCCTGCTTGCCTGACCCACCTGACCT
AACCTCTATTCCAGCACATTCC (SEQ ID NO : 78)

FIG. 5(3)

rMOR-1B2 (1628 bp)

MOR-1B2 (394 aa)

MDSSTGPGNTSDPLAQASCSPAPGSWLNLSHVDGNQSDPCGLNRRTGLGGNDSLCPQTGSPSMVTAITIMALYSIVCVVG
LFGNFLVMYVIVRYTKMKTATNIYIFNLALADALATSTILPFQSVNNYLMGTwPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRY
AVCHPVKALDFRTPRNAKIVNVCNWILSSAIGLPVMMFMATTKYRQGSIDCTLTFSHPTWYWEVNLKICVFIFAFIMPVLIITV
CYGLMLRILKSVRMLRRITRMVLVVVAVFIVCWTPIHIYVIKALITIPETTFQTVSWHFCIALGYTNNSCLNPVLRILPGMKTSSDA
SEEFCIPTSSSTIEQQNSTRVRQNTREHPSTANTVDRTRNHQEPQSVEI (SEQ ID NO:80)

FIG. 6A

rMOR-1C1 (1433 bp)

rMOR-1C1 (451 aa)

MDSSTGPGNTSDCSDPLAQASCSPAPGSWIQLSHVDGNQSDPCGLNRTGLGGNDSSLCPQRTGSPSMVTAITIMALYSIVVCVG
LFGNFLVMYVIVRYTKMKTATNIYIFNLALADALATSTLPFQSVNNYLMGTWPFGTILCKIVISIDYYNNMFTSIFTLCTMSVDRY
IAVCHPVKALDFRTPRNAKIVNVCNWILSSAIGLPVMMFMATTKYRQGSIDCTLTFSHPTTWYWENNLKICVFIFAFIMPVLIITV
CYGLMILRLKSVRMLSGSKEKDRNLRRITRMVLVVVAVFIVCWTPHIYVIIKAIITIPEITTFQTIVSWHFCIALGYTNSCLNPVLY
YAFLDENFKRCREFCIPTSSIEQQNSTVRQNTRTREHPSTANTVDRTNHQPALAVSVQAQIFTGYPSPTHGEKPCKSYRDRPRP
CGRTWSLJKSRAESNVEHEHCCGAALIYNNNNVNEI (SEQ ID NO:82)

FIG
6B

rMOR-1C2 (1480 bp)

GTACAGCCCTAGTCCGCAGCACGGCCATTCAACTGGACAGCAGGCCAGGAAACACCGAGCTGCTGGCTCAACTTGCCCCACCTGGCAAGTGGCAGGGAAACGGCACAGCTGCAGGCCATTACCATTCATGGCCCTCTACTCTATCGTGTGTAAGTGGCCCTTGGAAACTTCTGGTCATGTATGTGA
TTGTAAGATAACACAAATGAAAGACTGCCAACATCTACATTTCACCCCTAGGGACACAGTACACTGGCAACTACCTGTCAGAGTGTGATGGGAACATGGCCCTTCGGAACCATCCTCTGGCAAGATCGTGATCTCA
ATAGATTACTACAACATGTTCAACCAGCATATTCAACCGCATATTCAACCCCTGGATTCCCGTACCCCCCGAAATCGTCACCCAAATCGTCAACCCCA
CAGTCAAAGGCCCTGGATTCCGTATGGTCAATGTTCAACCAACCAAAATACAGGCAGGGCAGGGTCCATTAGATTGCAACCTGGATCCTCTGGCACC
CGGTCTGCCCTGGTAATGTTCAACCAACCTGGGAGAACCTGCTCAAACAAATCTGTCTTATCTGGCTTTCATCATGCCGGTCCCTCATCAGGGTCT
ACCTGGTACTGGGAGAACCTGCTCAAACAAATCTGTCTTATCTGGCTTTCATCATGCCGGTCCCTCATCAGGGTCT
TTACCGGCTGATGATGATCTTACGAACTCAAGAGCGGTTGGCATGGCTTACGAACTCAAGAGCGGTTGGCTGTATTATCGTCTGGACCCCC
GATCACCCCCGGATGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG
GGCCTGCTGATCACGATTCCAGAACACCATTCAGACCCGGTTGGCACTTCTGGCATTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG
GCCTGAATCCAGTTACGCCCTCCTGGATGAAAACCTCAAGCGATGCTCAGAGAGTTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG
ACGATCGAACAGCAAACACTCCAACTCGAGTCCGACTCGAGTCCGTCAGAACACTAGGGAACACTAGGGCTAACGGCTAACGGCTAAC
ACTAACCAACGCCAGCCCTGGCAGTCAGCGGTGGCCAGATCTTACAGGATACTCTCCGACTCATGGTGAAGAACATGGCTGGCTGGCTGG
CCTGCAAGAGTTACAGGGACAGACCTAGACCCCTGGAAAGAACGTGGCTTGAATGGCCAGTGGCTGGCTGGCTGGCTGGCTGGCTGG
AGCACCTCCATTGGGAGGCCGATTAATCTATAACAAATGAACAAAAATAGGGCCAGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG
GCACCGTGCCTGGCCCTGGTAATGAACACCGGGCTCCGATCTGAATAATCCTCTGTG (SEQ ID NO:83)

rMOR-1C2 (468 aa)

23/26

MDSSTGPGNNTSDCSDDPLAQASCPAPGSWLNLSHV DGNQSDPCCGLNRTGLGGNDSLCPQTGPSMSMVTAITIMALYSIVCVVG
LFGNFLVMYVIVRYTKMKKTATNIYIENLALADALATSTLFPQS VNVYLMGTWPFGTILCKIVISIDYNNMFTSIFTLC TMSVDRY
IAVCHPVKALDFRTPRNAKIVNVNWLSSAIGLPPVMFMATTKYRQGSIDCTLTFSHPTTWYWENLLKICVFI FAFIMPVLITV
CYGLMILRLKSVRMLSGSKEKDRNLRRJTRMVLVVVAVFIVCWTPIHIIYVIKALITIPETTFQTVSWHFCLALGYTNSCLNPVL
YAFLDENFKRCFREFCIPTSSTIEQQQNSTRVRQNTRHEPSTANTVDRTNHQPALAVSVAQIFTGYPSPTHGEKPCKSYRDRPRP
CGRTWSSLKSRAESNVEHHFCGAALIYNNELKIGPVSWLQMPAHLVVRPW (SEQ ID NO:84)

FIG. 6C

rMOR-1D (1385 bp)

rMOR-1D (387 aa)

MDSSSTGPGNTSDCSDPLAQASCSPAPGSWLNLSHVIDGNQSDPCGLNRRTGLGGNDSLCPQQTGSPSMVTAITIMALYSIVCVVG
LFGNFLVMYVIVRYTKMKTATNIYIFNLAIADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRY
IAVCHPVKALDFRTPRNAKIVNVCNWILSSAIGLPVMMATTKYRQGSIDCTLTFSHPTWYWWENLLKICVFVFAFIMPVLII
CYGLMILRLKSVRMLSGSKEKDRNLRRITRMVILVVVAVFIVCWTPIHIYVIKALITIPETTFQTVSWHFCIALGYTNSCLNPV
YAFLDENFKRCFREFCIPTSSTIEQQNSTRVRQNTRHPSSTANTVDRTNHQT (SEQ ID NO:86)

FIG. 6D

rMOR-1E (2078 bp)

FIG. 6E(1)

rMOR-1E (390 aa)

MDSSTGPGNTSDCSDPLAQASCSPAPGSWLNLSHVVDGNQSDPCGLNRTGGLGGNDSLCPQTGPSMVTAITIMALYSIVCVVG
LFGNFLVMYVIVRYTKMKTTATNIYIFNLALADALATSTLPFQSINYLMGTWPFEGTILCKIVISIDYYNNMFTSIFTLCTMSVSDRY
IAVCHPVVKALDFRTPRNAAKIVNVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLIKICVFIFAFIMPVLITV
CYGLMILRLKSVRMLSGSKEKDRLNRGITRMVLVVVAVFIIVCWTPIHYVIIKALITIPETTFQTVSWHFCIALGYTNNSCLNPVL
YAFLDENFKRCFREFCIPTSSTIEQQNSTRVRQNTREHPSTANTVDRTNHQGAEL (SEQ ID NO:88)

26/26

FIG. 6E(2)